

		Domain Ia									
		A ₀	B ₀	C ₀	D ₀						
TBEV E	281	SRCHLENRD	FVTGTGQTR	VTLVLEGGC	VTIYA-EGKP--S	MDV-WLDAIYQ	E	-----	-----	-----	-----
HCV E1	192				Y QVRNSSLGYH	VTNDC-----FNSS	VYTERADAILH	-----	-----	-----	-----
CSFV E2	689				GQLACK	EDRYAISST	NEIGLLGAGG	LATTWKEYNDLQL	NDGTVKICVAG	SPKVTALNVV	SRRYVLA
FUSION PEPTIDE											
		Domain Ila									
		a	b	c	d	e					
TBEV E	332	NP---AKTREY---	CL HAKLSDTKVA	ARCPYNGPAT	LAEEHQGGTV	CKRDQSDRGW	Q--NHCGL-FKKG	SIYACVKRAAC	EAKKKATGHV	YDAN	
HCV E1	223	TPGCVPCVREGNARCW	VA-VTPT-VA	TRGK-L-PTT	-----Q-----L	RRHIDLNVOS	A--TLCSALTY-G	DL--CGSVFL	VGQLFTFSR	HHWT	
CSFV E2	757	SLHKALPISVTFELLF	DGTNFTSEEM	EDDFGFLCP	PDTSPVVKGK	YNTT-LINGS	AFYLVCPFGW-TG	VI-ECTAV--	SP--TTL--R	TEVV	
		Domain Ib									
		F ₀	G ₀	H ₀							
TBEV E	416	KIVYTVKVED	HTGDYVAANE	THSGKRTAGF	TISSEKILT	NGEYGVVSL	CRVASGVDL	-----	-----	-----	-----
HCV E1	---	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
CSFV E2	---	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
		Domain Iib									
		f	g	h	i	j	k	l			
TBEV E	475	AQTVILELDK	TVEHLPTAQ	VHR-DWENDLA	LPWKHEGAQN	WNNARLVEF	GAPHAVKMDV	YNLGDQTCVL	LKALAGVFA	-HIEGKTIHL	KS
HCV E1	301	-----TQDC	NCSIYPGHIT	CHRMW-NMM	N-MSPTAAL-	-----VVAQLL	RIPQAI-MDM	I-AGAHMGVL	-----AGI----	-----K----	---
CSFV E2	842	-----K	TF--RRDKPF	PHRMDCVTTTV	ENEDLFYCKL	GGNWTGVK--	GEP-VVYTTGG	V-Y-KQCRWC	GPDENEPPDL	PHYPIGK----	---

Figure 1A

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Figure 1A cont.

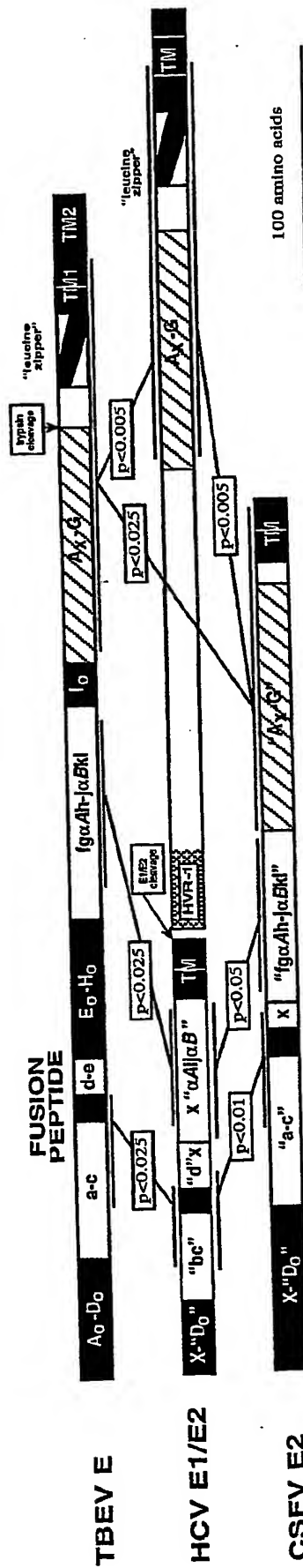


Figure 1B

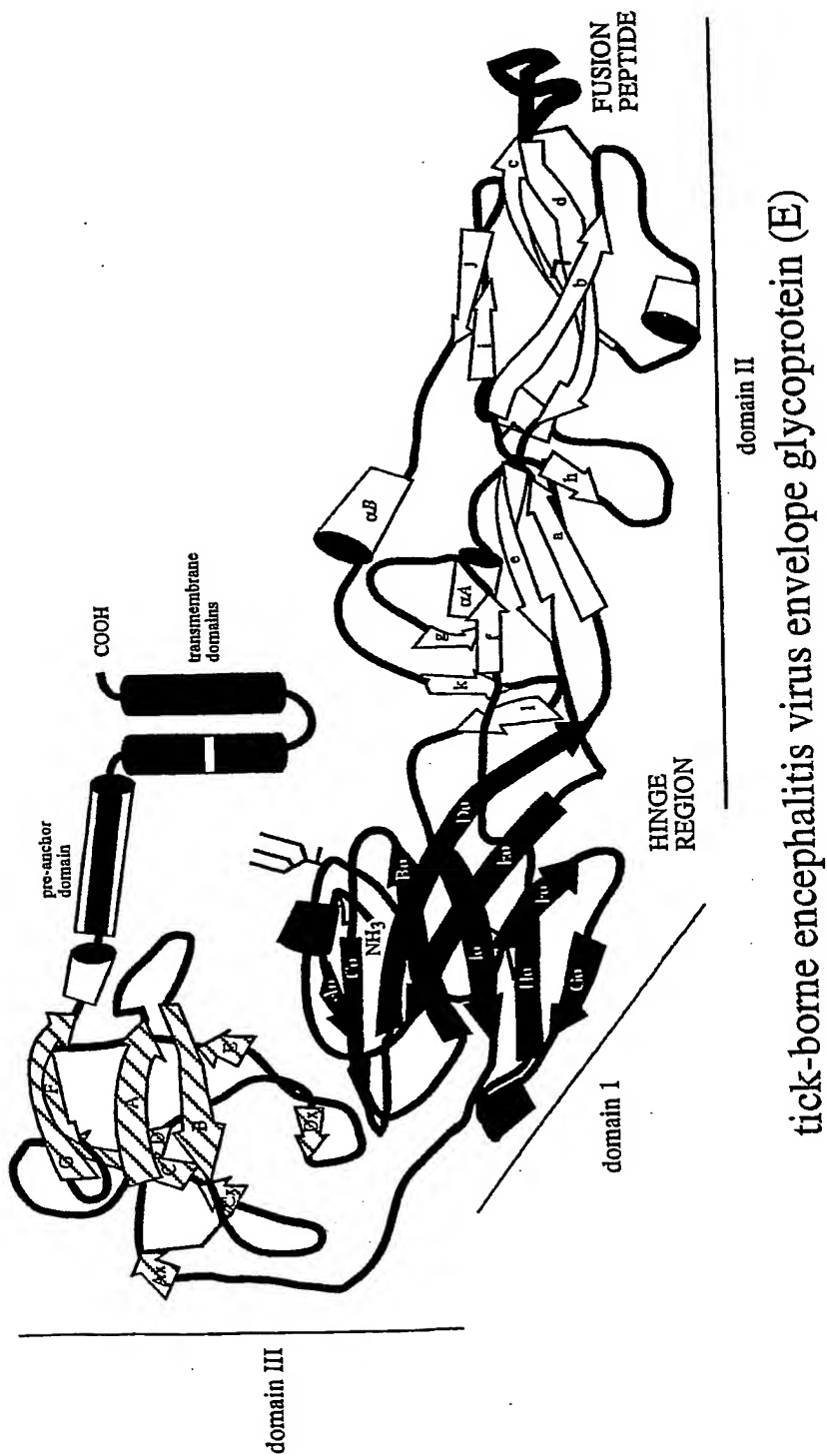


Figure 2

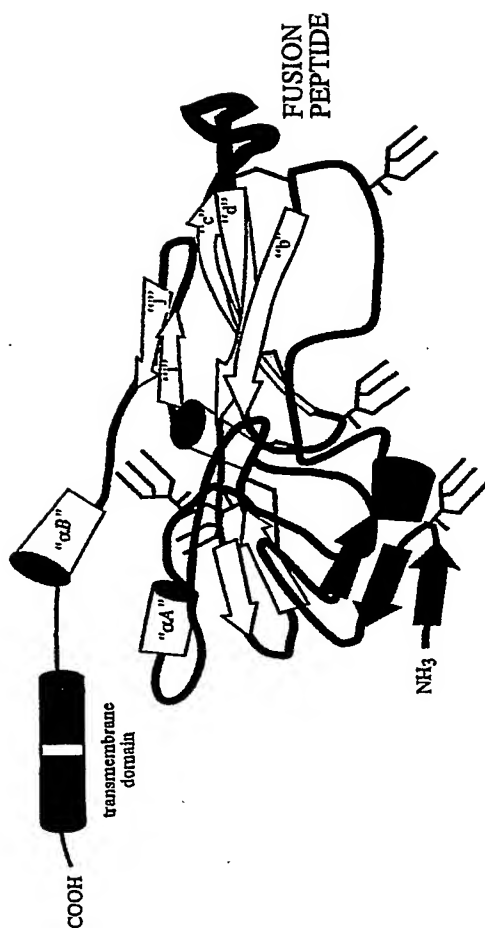


Figure 2 cont.



classic swine fever virus envelope glycoprotein 2 (E2)

Figure 2 cont.

A

TBEV prM	72	TLAATVRKER DGSTVIRAEG KDAATQVRVE NGTCVI--LATD MGSWCDDSL
CSFV E1	491	LSPYCN VTSKIGYIWTY TNNCTPACLP KN-TKIIGPG KFDNAEDGK ILHENGHLS-E FLLLSLVVLS
TBEV prM	164	-----YECVTIDQG-E EPVDVDCFCR NVDGVYLEYG RCGKQEGSRT RRSVLIPSHA-
CSFV E1	561	DFAPETASAL YLIFHYV-IPQSHE EPEGCDTNQL NLT-VEL-----RTEDVIPSSVW
TBEV prM	214	-QGELTGRGHK WLEGDSLRTH LTRVEGWVWK NKLLALAMVT VVWLTLESVV
CSFV E1	611	NVGKYYCVRPD WWPYETKVAL LFEEAGQVVK LALRALRDLT RWV---NSAS
TBEV prM	264	TRVAVLVVLL CLAPVYA
CSFV E1	659	TT-----AFLLI CLIKVLRGQIVQGVIM LLLVTGAQ

B

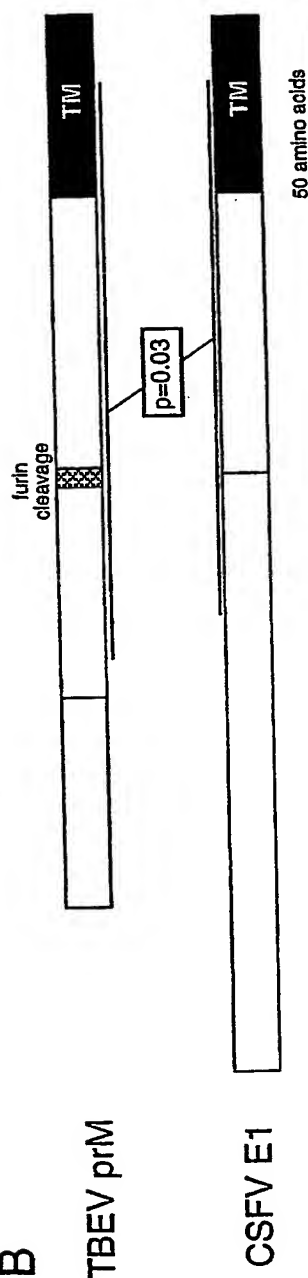


Figure 3

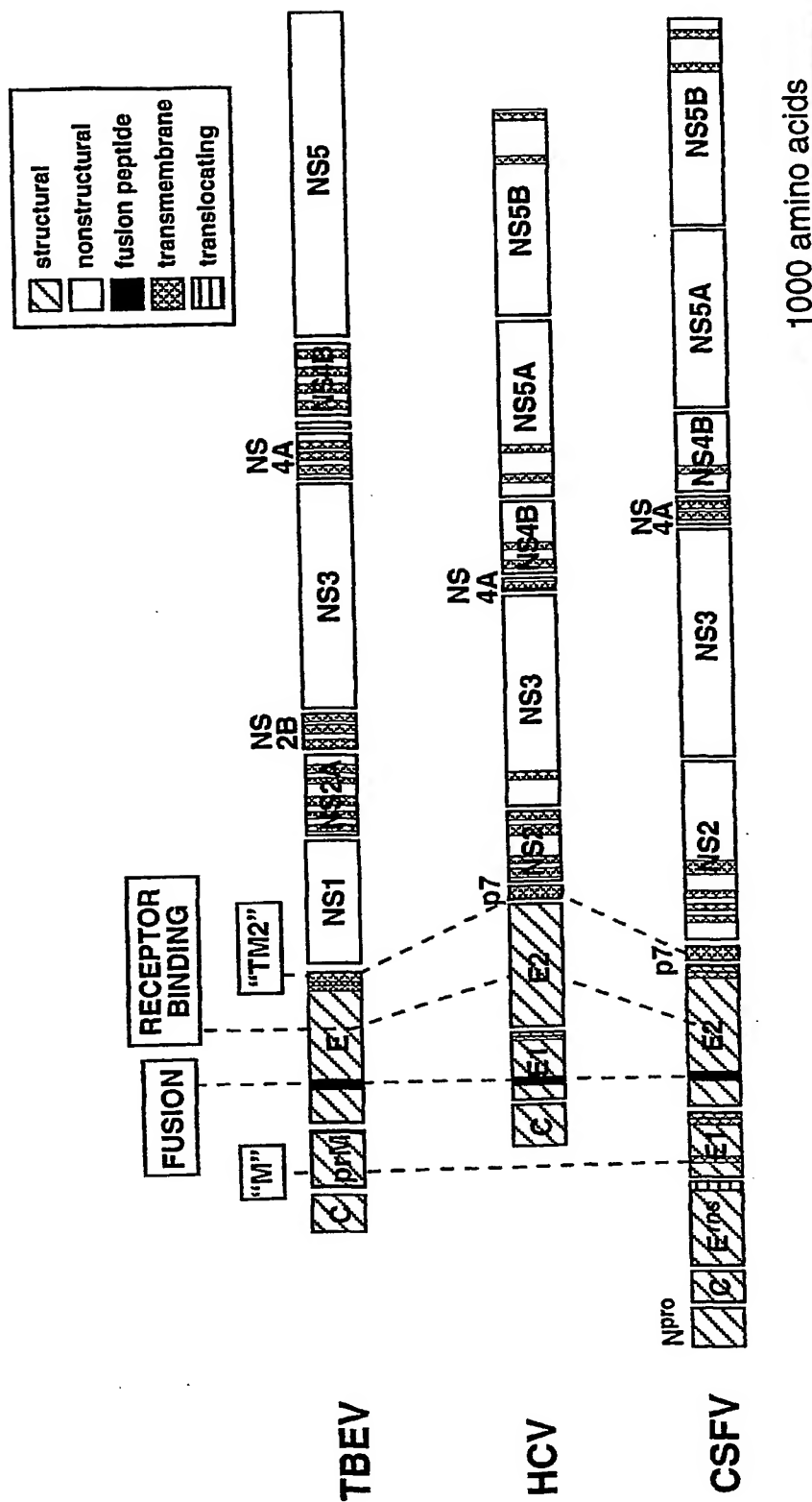


Figure 4

Figure 5

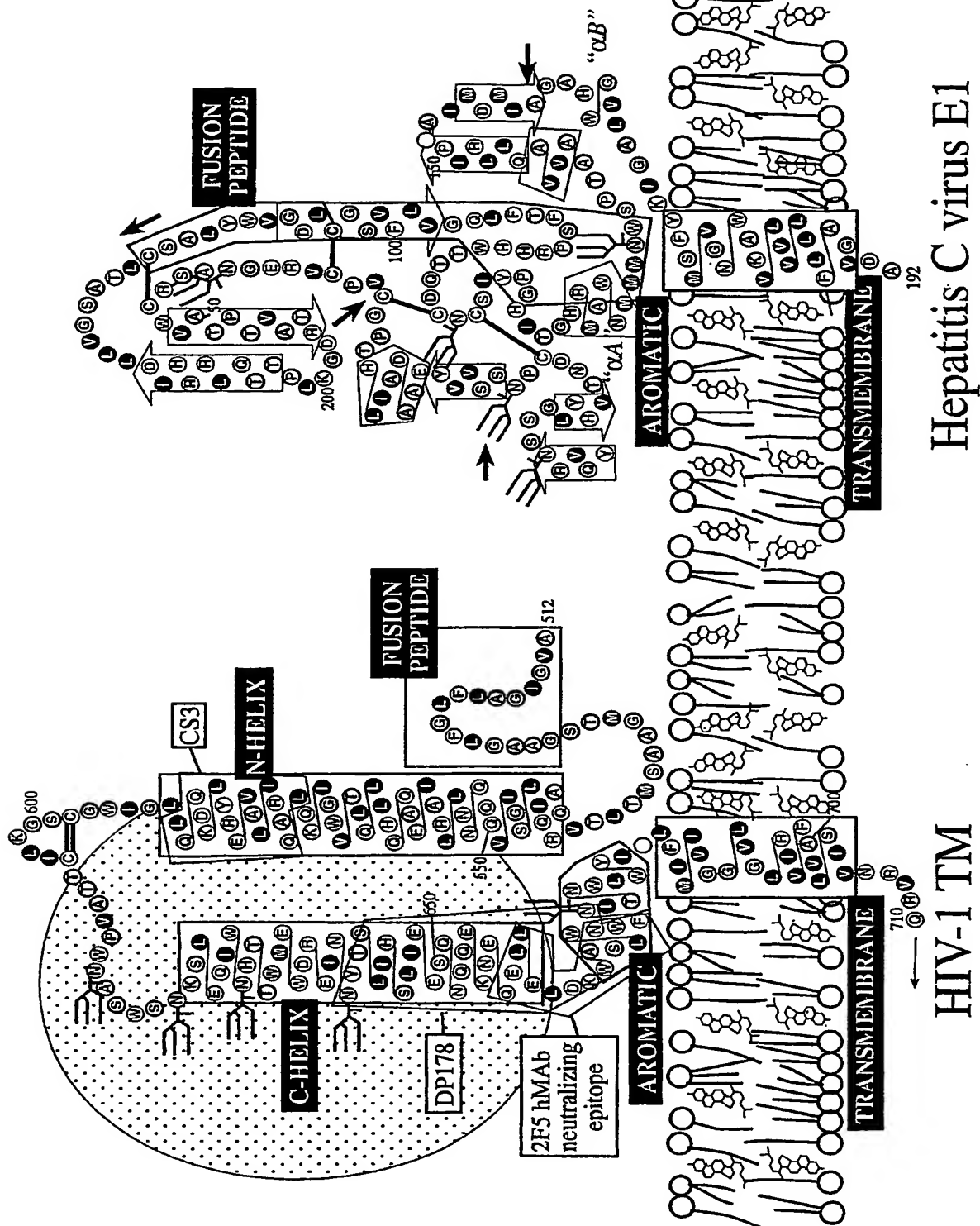


Figure 5